How do I submit **viral** sequences to GenBank?

Before you submit your data, you should determine the submission type and submission tool appropriate for that type.

⬇ Complete or Partial Viral Genomes

Bankit	tbl2asn
ncbi.nlm.nih.gov/WebSub/?tool=genbank	ncbi.nlm.nih.gov/genbank/tbl2asn2/
Web-based submission tool that provides forms for you to fill in the information necessary to submit your data.	Command line program that generates a valid submission from formatted files that contain the relevant sequence(s), source metadata, and annotation tables.

⬇ Influenza A, B or C

Submission Portal

submit.ncbi.nlm.nih.gov/subs/genbank/

Online wizard submission tool that provides immediate validation and feedback and adds coding region and gene annotation for you. We plan to add other viruses in the future.

⬇ Unassembled sequence reads from a viral sample, a metagenome, or a metatranscriptome

Sequence Read Archive (SRA)

ncbi.nlm.nih.gov/Traces/sra_sub/sub.cgi?&m=submissions&s=defaults

Accepts genetic data and the associated quality scores produced by next generation sequencing technologies.

🚫 Complete viral genomes and viral assemblies should **not** be submitted via the **Whole Genome Shotgun (WGS)** pathway.

Submission checklist

- ☼ **Authors submitting the data**
- ☼ **Associated publication**
- ☼ **Nucleotide sequence(s) in FASTA format**
- ☼ **Annotation of coding regions, genes and any other relevant information**
  - **Annotation in BankIt and tbl2asn**
    - Important for users and to validate sequence quality
    - Coding regions should be added even if sequence is partial
    - Provide annotation in 5-column feature table or in Bankit online forms
    - More info on table format at ncbi.nlm.nih.gov/Sequin/table.html
- ☼ **Source metadata**
  - scientific name of the virus
  - isolate or strain designation
  - serotype or genotype if appropriate
  - segment name/number if appropriate
  - country where the virus was isolated
  - host and/or physical environment from which virus was isolated
  - complete collection date, including month and day if known

Submission Tips

Release Date for your sequence can be immediately after processing, or you can choose a later date.
- The release date can be changed after submission, for example if your publication is published earlier than expected (congrats!).

Not sure what "organism" you should choose?
Need a template for annotation? Try doing a BLASTn or tBLASTx search.
- Limit results to viral RefSeqs: Next to "Database," choose "Reference genomic sequences (refseq_genomic)," and next to "organism" type to select "Viruses (taxid: 10239)."
- The GenBank record for closely-related RefSeqs can give you taxonomic information, including the appropriate "organism" term. To get an example of annotation, click "Send to" on the top right, select "Complete record" and "File," and for the format select "Feature table."
- The ICTV often provides similarity cutoffs for viral groups, which may give you an idea of the taxonomic classification of your virus.

Help NCBI improve resources for your favorite virus.
Write to us at **info@ncbi.nlm.nih.gov** and let us know.